

# Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

## STAFF USE ONLY

Searcher: car

Searcher Phone #: 2-2504

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: 1/8/05

Date Completed: 1/8/05

Searcher Prep: Review Time \_\_\_\_\_

Clerical Prep Time: 10

Online Time: 415

## Type of Search

NA Sequence (#) ✓

AA Sequence (#) ✓

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other \_\_\_\_\_

## Vendors and cost where applicable

STN \_\_\_\_\_

Dialog \_\_\_\_\_

Questel/Orbit \_\_\_\_\_

Dr.Link \_\_\_\_\_

Lexis/Nexis \_\_\_\_\_

Sequence Systems ✓

WW/Internet \_\_\_\_\_

Other (specify) \_\_\_\_\_



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 141839**

**TO: Ilia Ouspenski**  
**Location: 3d74 / 3c70**  
**Saturday, January 08, 2005**  
**Art Unit: 1644**  
**Phone: 272-2920**  
**Serial Number: 10 / 008264**

**From: Jan Delaval**  
**Location: Biotech-Chem Library**  
**Rem 1a51**  
**Phone: 272-2504**  
  
**jan.delaval@uspto.gov**

### **Search Notes**

QY 1201 GCAGTCAGATGAGAGCTGATCTTCTGCGCTGCTGCGCCCACTGCTCTACTAC 1260  
 DB 1412 GCAGTCAGATGAGAGCTGATCTTCTGCGCTGCTGCGCCCACTGCTCTACTAC 1471  
 QY 1261 GCAGTCAGATGAGAGCTGATCTTCTGCGCTGCTGCGCCCACTGCTCTACTAC 1320  
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RESULT 7  
 AF093098 2589 bp mRNA linear PRI 06-DEC-2000  
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 AF093098  
 ACCESSION AF093098.1 GI:6002604  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS  
 TITLE  
 Zhang, W.X. and Yang, S.Y.  
 Cloning and characterization of a new member of the T-box gene family

JOURNAL  
 MEDLINE  
 PUBMED  
 20541708  
 11087660  
 2 (bases 1 to 2589)

REFERENCE  
 AUTHORS  
 TITLE  
 Yang, S.  
 Direct Submission  
 Submitted (17-SEP-1998) Molecular Immunogenetics Lab, New York  
 Medical College, 19 Bradhurst Ave, Hawthorne, NY 10532, USA  
 Location/Qualifiers  
 1. 2589

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 /db\_xref="GI:6002605"  
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 KQGRWPPFLSTVAGLEPTSHYRMFVDVVLVDQHWRYSGKRVYCGKABGSMFGR

## ORIGIN

Query Match 100.0%; Score 1608; DB 9; Length 2589;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-252;  
 Matches 1608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCATCTGAGAGAGCGGGTTCGCGAATCTGCTGAGCGGCACTGCGCGG 60  
 DB 212 ATGGCATCTGAGAGAGCGGGTTCGCGAATCTGCTGAGCGGCACTGCGCGG 271  
 QY 61 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
 DB 212 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 331  
 QY 272 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 DB 332 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 391  
 QY 181 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
 DB 392 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 451  
 QY 241 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
 DB 452 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 511  
 QY 301 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
 DB 512 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 571  
 QY 361 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
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 DB 932 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 991  
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 DB 992 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1051  
 QY 841 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900  
 DB 1052 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1111  
 QY 901 AGCGACGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 6, 2005, 06:07:23 ; Search time 196 seconds

(without alignments)  
1570.538 Million cell updates/sec

Title: US-10-008-264a-2

Perfect score: 2942  
Sequence: 1.MGIVEPCGDMLTGTETPMG.....GAPSPFDKAEAGQFYNYFPN 535

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02:.\*  
1: uniprot\_trembl:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2942	100.0	535	1 TX21_HUMAN	Q91117 homo sapien
2	2570.5	87.4	530	2 Q9ROA6	Q9ROA6 mus musculu
3	2565.5	87.2	530	2 Q9JXK8	Q9JXK8 mus musculu
4	1175	39.9	223	2 Q80X15	Q80X15 peromyscus
5	970	33.0	669	2 Q9PVX6	Q9PVX6 cynops pyrr
6	968	32.9	707	2 Q8BN22	Q8BN22 mus musculu
7	959.5	32.6	692	1 E0WD_XENLA	P79944 xenopus lae
8	945.5	32.1	688	1 E0WD_MOUSE	Q54839 mus musculu
9	943.5	32.1	688	2 Q9JTL1	Q9JTL1 mus musculu
10	937	31.8	661	2 Q9RTU2	Q9RTU2 brachydanio
11	937	31.8	661	2 Q9DDU3	Q9DDU3 brachydanio
12	937	31.8	661	2 AAH67719	AAH67719 brachydanio
13	927.5	31.5	686	1 E0WD_HUMAN	Q95936 homo sapien
14	927.5	31.3	681	1 TBRI_MOUSE	Q64336 mus musculu
15	921.5	31.3	681	2 Q7TSY9	Q7TSY9 mus musculu
16	921.5	31.3	681	2 AAH58399	AAH58399 mus muscu
17	921.5	31.3	682	1 TBRI_HUMAN	Q16650 homo sapien
18	751	25.5	624	2 Q966R5	Q966R5 brachydanio
19	742.5	25.2	437	2 Q9DDU4	Q9DDU4 brachydanio
20	735	25.0	640	2 Q9GRF2	Q9GRF2 ptychodera
21	735	25.0	663	2 Q9GQ84	Q9GQ84 brachydanio
22	706	24.0	193	2 Q6SUT9	Q6SUT9 rattus norv
23	706	24.0	193	2 AAH21241	AAH21241 rattus no
24	626.5	20.7	939	2 Q9GR40	Q9GR40 hemelcentro
25	609.5	20.4	958	2 Q9NLA40	Q9NLA40 asterina pe
26	600.5	19.9	116	2 Q8UTAS	Q8UTAS marimota mon
27	585	19.9	116	2 Q8UTAS	Q8UTAS marimota mon
28	578.5	19.7	554	1 TBX4_CANFA	P85109 canis famli
29	573	19.5	545	1 TBX4_HUMAN	P70327 mus musculu
30	569.5	19.4	540	1 TBX6_MOUSE	Q24432 drosophila
31	559	19.0	972	1 OMH_DROME	

32	558.5	19.0	436	1 TBX6_HUMAN	Q95947 homo sapien
33	558	19.0	552	1 TBX4_MOUSE	P70325 mus musculu
34	556.5	18.9	479	2 Q99P22	Q99P22 mus musculu
35	554.5	18.8	488	2 Q99MP0	Q99MP0 mus musculu
36	552	18.8	541	2 Q93288	Q93288 gallus gall
37	551	18.7	519	2 Q9W7C2	Q9W7C2 xenopus lae
38	551	18.7	701	1 TBX2_MOUSE	Q60707 mus musculu
39	549	18.7	518	1 TBX5_HUMAN	Q95933 homo sapien
40	544.5	18.5	697	1 BYN_DROME	P55965 drosophila
41	541	18.4	492	2 Q91AK8	Q91AK8 brachydanio
42	540	18.4	372	2 Q9PTK3	Q9PTK3 brachydanio
43	538	18.3	485	2 Q9PU87	Q9PU87 brachydanio
44	537.5	18.3	702	2 Q63AK2	Q63AK2 canis famli
45	536.5	18.2	454	2 Q70HR6	Q70HR6 podocoryne

## ALIGNMENTS

RESULT 1  
TX21\_HUMAN STANDARD, PRT, 535 AA.  
AC Q9JTL1:  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE T-box transcription factor TBX21 (T-box protein 21) (Transcription factor TBX21) (T-cell-specific T-box transcription factor T-bet).  
GN Name=TBX21; Synonyms=TBX21, TBET;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yang S.;  
RT "Cloning and characterization of a new member of T-box gene family.";  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Szabo S.J.; Kim S.T.; Costa G.L.; Zhang X.; Fathman C.G.;  
RA Glimcher L.H.;  
RT "A novel transcription factor, T-bet, directs Th1 lineage commitment.";  
RL Cell 100:655-669(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=20222568; PubMed=10761931;  
RA MEDLINE=20222568; PubMed=10761931;  
RA Szabo S.J.; Kim S.T.; Costa G.L.; Zhang X.; Fathman C.G.;  
RA Glimcher L.H.;  
RT "A novel transcription factor, T-bet, directs Th1 lineage commitment.";  
RL Cell 100:655-669(2000).  
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RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straube R.L.; Feingold B.A.; Grouse L.H.; Derge J.G.;  
RA Klausner R.D.; Collins P.S.; Wagner L.; Shemen C.M.; Schuler G.D.;  
RA Ahschul S.F.; Zeeberg B.; Buelow K.H.; Schaefer C.F.; Bhat N.K.;  
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh P.;  
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;  
RA Stappleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schetz T.B.;  
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carrinot P.; Prange C.;  
RA Rana S.S.; Loquellano N.A.; Peters G.J.; Adamson R.D.; Mullany S.J.;  
RA Roark S.A.; McKernan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;  
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;  
RA Villalón D.K.; Muzny D.M.; Sodergren B.J.; Lu X.; Gibbs R.A.;  
RA Rahay J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;  
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;  
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;  
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;  
RA Buterfield Y.S.N.; Krzywinski M.I.; Skalska U.; Smallus D.B.;  
RA Scherch A.; Schein J.R.; Jones S.J.M.; Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Transcription factor that controls the expression of the Th1 cytokine, interferon-gamma. Initiates Th1 lineage development from naive Th precursor cells both by activating Th1 genetic

CC programs and by repressing the opposing TH2 programs.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- TISSUE SPECIFICITY: T-cell specific.  
 CC -1- SIMILARITY: Contains 1 T-box domain.  
 CC -----  
 CC This SMYD8-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@1sb-eb.ch](mailto:license@1sb-eb.ch)).  
 CC -----  
 CC EMBL; AF093098; AAF00055.1; -  
 CC EMBL; AF241243; AAF61243.1; -  
 CC EMBL; BC039739; AAH39739.1; -  
 CC HSSP; P24781; 1XBR.  
 CC TRANSFAC; T04948; -  
 CC DR Genew; HGNC; 11599; TBX21.  
 CC DR MIM; 604895; -  
 CC DR GO; GO:0005634; C:nucleus; NAS.  
 CC DR GO; GO:0003700; P:transcription factor activity; TAB.  
 CC DR GO; GO:0007275; P:development; TAB.  
 CC DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; TAB.  
 CC DR InterPro; IPR008967; P53 like DNA\_Bnd.  
 CC DR InterPro; IPR001699; TF\_T-box.  
 CC DR Pfam; PF00907; T-box; 1.  
 CC DR PRINTS; PR00937; TBOX. 1.  
 CC DR SMART; SM00425; TBOX. 1.  
 CC DR PROSITE; PS01283; TBOX\_1; 1.  
 CC DR PROSITE; PS01264; TBOX\_2; 1.  
 CC DR PROSITE; PS0252; TBOX\_3; 1.  
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 Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 421 RQGEVTLAPGAGWVAPQYPPKMGASFRPMTLPMRPGSGSGRBPBOGPIVWTEI 480  
 QY 421 RQGEVTLAPGAGWVAPQYPPKMGASFRPMTLPMRPGSGSGRBPBOGPIVWTEI 480  
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DB 481 APTRPSSDSGLGKSDSKRRRVSPYSSGDSPPAGAPSPFDKABQGFYNYFPN 535  
 RESULT 2  
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 AC Q9R0A6  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
 DE Transcription factor TBLX1.  
 GN Name=Tbx21; Synonyms=Tblym;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=20541708; PubMed=11087660;  
 RA Zhang, Wx, Yang S.Y.;  
 RT "Cloning and characterization of a new member of the T-box gene  
 RT family.";  
 RL Genomics 70:41-48 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Yang S.Y.  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF093099; AAF00056.1; -  
 DR HSSP; P24781; 1XBR.  
 DR MGD; MGI:1888984; Tbx21.  
 DR GO; GO:004304; P:positive regulation of isotype switching to..; IMP.  
 DR GO; GO:0050776; P:regulation of immune response; IMP.  
 DR InterPro; IPR008967; P53 like DNA\_Bnd.  
 DR InterPro; IPR001699; TF\_T-box.  
 DR Pfam; PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX. 1.  
 DR SMART; SM00425; TBOX. 1.  
 DR PROSITE; PS01283; TBOX\_1; 1.  
 DR PROSITE; PS01264; TBOX\_2; 1.  
 DR PROSITE; PS0252; TBOX\_3; 1.  
 SQ SEQUENCE 530 AA; 57841 MW; 05AF84B6A227FE8 CRC64;  
 Query Match 87.4%; Score 2570.5; DB 2; Length 530;  
 Best Local Similarity 87.1%; Pred. No. 2, 1e-137;  
 Matches 466; Conservative 24; Mismatches 40; Indels 5; Gaps 2;  
 QY 1 MGIVRGCGDMLTGTETPMGSDGGRAPADPQHRFYPPRGAODADRRGGSLGSPYPG 60  
 DB 1 MGIVRGCGDMLTGTETPMGSDGGRAPADPQHRFYPPRGAODADRRGGSLGSPYPG 60  
 DB 1 MGIVRGCGDMLTGTETPMGSDGGRAPADPQHRFYPPRGAODADRRGGSLGSPYPG 60  
 QY 61 GALVPAAPSRFLGAVYPPRPOAAGPPGAGSPPPADAGYOPGEGYAAPDRAGLYPG 120  
 DB 61 GALVPAAPSRFLGAVYPPRPOAAGPPGAGSPPPADAGYOPGEGYAAPDRAGLYPG 120  
 DB 61 GALVPAAPSRFLGAVYPPRPOAAGPPGAGSPPPADAGYOPGEGYAAPDRAGLYPG 120  
 QY 121 PREDYALPAGLEVSGLRLVALNNHLLMSKENQHOTEMITTKGRMPPLSLFTVAGLEPT 180  
 DB 121 PREDYALPAGLEVSGLRLVALNNHLLMSKENQHOTEMITTKGRMPPLSLFTVAGLEPT 180  
 QY 121 PREDYALPAGLEVSGLRLVALNNHLLMSKENQHOTEMITTKGRMPPLSLFTVAGLEPT 180  
 DB 121 PREDYALPAGLEVSGLRLVALNNHLLMSKENQHOTEMITTKGRMPPLSLFTVAGLEPT 180  
 QY 120 PREDYALPAGLEVSGLRLVALNNHLLMSKENQHOTEMITTKGRMPPLSLFTVAGLEPT 179  
 DB 120 PREDYALPAGLEVSGLRLVALNNHLLMSKENQHOTEMITTKGRMPPLSLFTVAGLEPT 179  
 QY 181 SHTRMFVDVVLVDQHHMRVQSGKRVQCGKAGSMGPNRLYVHPDSPTNGAHMRQVSVFG 240  
 DB 181 SHTRMFVDVVLVDQHHMRVQSGKRVQCGKAGSMGPNRLYVHPDSPTNGAHMRQVSVFG 240  
 QY 181 SHTRMFVDVVLVDQHHMRVQSGKRVQCGKAGSMGPNRLYVHPDSPTNGAHMRQVSVFG 240  
 DB 181 SHTRMFVDVVLVDQHHMRVQSGKRVQCGKAGSMGPNRLYVHPDSPTNGAHMRQVSVFG 240  
 QY 241 KKLITNNKASNNVTOMITVLSLHKYQPRLIHVEVNDGEBRAACNANTHTIPTFOETOFI 300  
 DB 241 KKLITNNKASNNVTOMITVLSLHKYQPRLIHVEVNDGEBRAACNANTHTIPTFOETOFI 300  
 QY 241 KKLITNNKASNNVTOMITVLSLHKYQPRLIHVEVNDGEBRAACNANTHTIPTFOETOFI 300  
 DB 241 KKLITNNKASNNVTOMITVLSLHKYQPRLIHVEVNDGEBRAACNANTHTIPTFOETOFI 300  
 QY 240 KKLITNNKASNNVTOMITVLSLHKYQPRLIHVEVNDGEBRAACNANTHTIPTFOETOFI 299  
 DB 240 KKLITNNKASNNVTOMITVLSLHKYQPRLIHVEVNDGEBRAACNANTHTIPTFOETOFI 299  
 QY 301 AATAYONAEITTKIDNNPPAKGFRENFSNTSVDTSIPSPGPNCOPLGSDHYSLPLP 360  
 DB 301 AATAYONAEITTKIDNNPPAKGFRENFSNTSVDTSIPSPGPNCOPLGSDHYSLPLP 360  
 QY 301 AATAYONAEITTKIDNNPPAKGFRENFSNTSVDTSIPSPGPNCOPLGSDHYSLPLP 360  
 DB 301 AATAYONAEITTKIDNNPPAKGFRENFSNTSVDTSIPSPGPNCOPLGSDHYSLPLP 360  
 QY 300 AATAYONAEITTKIDNNPPAKGFRENFSNTSVDTSIPSPGPNCOPLGSDHYSLPLP 359  
 DB 300 AATAYONAEITTKIDNNPPAKGFRENFSNTSVDTSIPSPGPNCOPLGSDHYSLPLP 359